Amendments to the Specification:

Please amend the paragraph on page 5, lines 12-23 as follows:

The gene products implicated in *Salmonella* pathogenesis include type three secretion systems (TTSS), proteins affecting cytoplasmic structure of the target cells, many proteins carrying out functions necessary for survival and proliferation of *Salmonella* in the host, as well as "traditional" factors such as endotoxin and secreted exotoxins. Additionally, there must be factors mediating species-specific illnesses. Despite this most of the genomes of *S. enterica* ser. Typhi (see http://www.sanger.ac.uk/Projects/S_typhi/ ~~http://www.sanger.ac.uk/Projects/S_typhi/~~ for the genome database) and *S. enterica* ser. Typhimurium (see http://genome.wustl.edu/gsc/bacterial/salmonella.shtml ~~http://genome.wustl.edu/gsc/bacterial/salmonella.shtml~~ for the genome database) are highly conserved and are mutually useful for gene identification in multiple serovars. The Salmonella are a complex group of enteric bacteria causing disease similar to but distinct from other gram-negative enterics such as *E. coli* and have been a focus of biomedical research for the last century.

Please amend the paragraph on page 75, line 22 to page 76, line 17 as follows:

By "homologous coding nucleic acid" is meant a nucleic acid homologous to a nucleic acid encoding a gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 8-3795 or a portion thereof. In some embodiments, the homologous coding nucleic acid may have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. In other embodiments the homologous coding nucleic acids may have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequences complementary to one of SEQ ID NOs.: 8-3795 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Identity may be measured using BLASTN version 2.0 with the default parameters or tBLASTX

with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its entirety) Alternatively a "homologuous coding nucleic acid" could be identified by membership of the gene of interest to a functional orthologue cluster. All other members of that orthologue cluster would be considered homologues. Such a library of functional orthologue clusters can be found at http://www.ncbi.nlm.nih.gov/COG ~~http://www.ncbi.nlm.nih.gov/COG~~. A gene can be classified into a cluster of orthologous groups or COG by using the COGNITOR program available at the above web site, or by direct BLASTP comparison of the gene of interest to the members of the COGs and analysis of these results as described by Tatusov, R.L., Galperin, M.Y., Natale, D. A. and Koonin, E.V. (2000) The COG database: a tool for genome-scale analysis of protein functions and evolution. Nucleic Acids Research v. 28 n. 1, pp33-36.

Please amend the paragraph on page 89, line 28 to page 90, line 19 as follows:

In one embodiment of the present invention, an operon is identified and then dissected to determine which gene or genes are required for proliferation. Operons can be identified by a variety of means known to those in the art. For example, the RegulonDB DataBase described by Huerta et al. (*Nucl. Acids Res.* 26:55-59, 1998), which may also be found on the website http://www.cifn.unam.mx/Computational_Biology/regulondb/ , the disclosures of which are incorporated herein by reference in their entireties, provides information about operons in *Escherichia coli*. The Subtilist database (http://bioweb.pasteur.fr/GenoList/SubtiList), (Moszer, I.; Glaser, P. and Danchin, A. (1995) Microbiology 141: 261-268 and Moszer, I (1998) FEBS Letters 430: 28-36, the disclosures of which are incorporated herein in their entireties), may also be used to predict operons. This database lists genes from the fully sequenced, Gram-positive bacteria, *Bacillus subtilis*, together with predicted promoters and terminator sites. This information can be used in conjunction with the *Staphylococcus aureus* genomic sequence data to predict operons and thus produce a list of the genes affected by the antisense nucleic acids of the present invention. The *Pseudomonas aeruginosa* web site (http://www.pseudomonas.com) can be used to help predict operon organization in this bacterium. The databases available from the Genome Sequencing Center (http://genome.wustl.edu/gsc/salmonella.shtml), and the Sanger

Centre (http://www.sanger.ac.uk/projects/S___typhi) may be used to predict operons in *Salmonella typhimurium*. The TIGR microbial database has an incomplete version of the *E. faecalis* genome http://www.tigr.org/cgi-bin/BlastSearch/blast.cgi?organism=e_faecalis ~~http://www.tigr.org/cgi-bin/BlastSearch/blast.cgi?organism=e_faecalis~~. One can take a nucleotide sequence and BLAST it for homologs.

Please amend the paragraph on page 184, line 21 to page 185, line 5 as follows:

As a demonstration of the methodology required to find homologues to an essential gene, nine prokaryotic organisms were analyzed and compared in detail. First, the most reliable source of gene sequences for each organism was assessed by conducting a survey of the public and private data sources. The nine organisms studied are *Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus, Streptococcus pneumoniae* and *Salmonella typhi.* Full-length gene protein and nucleotide sequences for these organisms were assembled from various sources. For *Escherichia coli, Haemophilus influenzae* and *Helicobacter pylori,* gene sequences were adopted from the public sequencing projects, and derived from the GenPept 115 database (available from NCBI). For *Pseudomonas aeruginosa*, gene sequences were adopted from the Pseudomonas genome sequencing project (downloaded from http://www.pseudomonas.com ~~http://www.pseudomonas.com~~). For *Klebsiella pneumoniae, Staphylococcus aureus, Streptococcus pneumoniae* and *Salmonella typhi,* genomic sequences from PathoSeq v 4.1 (Mar 2000 release) was reanalyzed for ORFs using the gene finding software GeneMark v 2.4a, which was purchased from GenePro Inc. 451 Bishop St., N.W., Suite B, Atlanta, GA, 30318, USA.